

Fig. 1

1 AGCTCACAGCC 11
 12 ATGGTTACCTTCAGCCACGTCTCCAGTCTGAGTCACTGGTTCCTCTTGCTGCTGCTGCTG 71
 1 M V T F S H V S S L S H W F L L L L L L 20
 72 AATCTGTTCTTGCCGGTAATATTTGCTATGCCTGAATCATACTCCTTCAACTGTCCCGAT 131
 21 N L F L P V I F A M P E S Y S F N C P O 40
 132 GGTGAATACCAGTCTAATGATGTCTGTTGCAAGACCTGTCCCTCAGGTACATTTGTCAAG 191
 41 G E Y Q S N D V C C K T C P S G T F V K 60
 192 GCGCCCTGCAAAATCCCCCATACTCAAGGACAATGTGAGAAGTGTACCCAGGAACATTC 251
 61 A P C K I P H T Q G Q C E K C H P G T F 80
 252 ACAGGGAAGATAATGGCCTGCATGATTGTGAACTTTGCTCCACCTGTGATAAAGACCAG 311
 81 T G K D N G L H D C E L C S T C D K D Q 100
 312 AATATGGTGCTGACTGTTCTGCCACCAGTGACCGGAAATGCGAGTGCCAAATAGGTCTT 371
 101 H M V A D C S A T S D R K C E C Q I G L 120
 372 TACTACTATGACCCAAAATTTCCGGAATCATGCCGCCCATGTACCAAGTGTCCCAAGGA 431
 121 Y Y Y D P K F P E S C R P C T K C P Q G 140
 432 ATCCCTGTCTCCAGGAATGCAACTCCACAGCTAACACTGTGTGCAGTTTCTCTGTTTCA 491
 141 I P V L Q E C N S T A N T V C S S S V S 160
 492 AATCCCAGAACTGGCTGTTCTACTGATGCTAATTGTCTTCTGTATCTGA 542
 161 N P R N W L F L L M L I V F C I * 177
 543 AGAAGATAAGGTTCTACAGATGGTGTCTGTAGCTTCCTTTTATTGCTGTGAAGAGAA 600
 601 ACCATGGAGGCAACTCTTTCATTTTATTTTATTTTAAATGTCTTGAACCTGATTGAAG 660
 661 ACCAGGCTGGACTCAAACTCACAGAGATCCGGACTAGGCACCTCTAATATAGGAAAACAT 720
 721 TGAATTGGGACTGGCTTACAGTTTCAAGATTCTGTCCATGATTATCATAGTGGGAAGCA 780
 781 TGGAGGCACGGAGGCACACATGGTGCTGGAGAAGAAGCTGAGAGTTCTGCATCTTGATCT 840
 841 GCAAGCAATAAAGGAGACTGTGTGCCACACTACACATAGCTTGAACATAGGAGACCTCA 900
 901 AAGCTGTCCCCACAGTGACAACTTCTCCAACAAGGTATACCTCCTAATAATACCAT 960
 961 TTCTTATGAGGCAAGCATTCAAACACATGAGTCTATGAGGGCCAAACCAATTCAAACCA 1020
 1021 CACAGGTTAACAATTGCCCTCTGCAGCTCTCTGGTGGAGGCCCTCCTTGAGAGTAAGTAA 1080
 1081 CAATTTAGATGAAGGCAAGTCTGATCAGGTCCAAAAGAACTCAGGATGAATGGTCC 1140
 1141 ACTGTGGTTCTTATTAACATACTGAAGAACATGACCTCACCTTAGACTTCTCCACCTCAC 1200
 1201 TGGCTTCCCTTCCCCTAGCTTCTCATTCCCAGGTAACCCTGCCATTTTTTGGTAATGTGC 1260
 1261 CTTCTTGGTTCTTCTCTCTCTTCCCCCTCTCTTCTGGTCTTATTTCTTCTCTCTCCC 1320
 1321 ACTCTCCACCAGCCGCTCTTAAGGCCTGAGTCAGTCTGAGGCCATGTTTAATCTACTA 1380
 1381 CTTTCTCTCTGCTCTGGACTCATCCAGATGTCTCTGGCTGAGCTCTCCCTCTATCTACA 1440
 1441 ATAAAACCTTCCCCTAACAGAAATGGAAACAGTTTTGCTCTCACTTTGTACATCTGGTG 1500
 1501 CCTGAAACC 1509

Fig. 2

7F4 GPDGEY---QSDVQ CKTGPSGTFVKAPCK IPHTQQGCEKCHPGT FTGKDNGLHDGELCS 60
mTNFR CPGGKYVHSHKNSIG GTKCHKGTLYLVSDCP SPGRDTCRECEKGT FTASQNYLRQCLSCK 60

7F4 TGDKD--QNMVADCS ATSDRKCEG---QIG LYYYPKFPESGRPC TKCPQGIPVLQEGNS 120
mTNFR TCRKEMSQVEISPCQ ADKDTVCGCKENQFQ RYLSETHFQ--GVDC SPCFNGTVTIP-GKE 120

7F4	<u>TANTVC</u>	126
7F4	TNFR TQNTVC	126

Fig. 3

testis

kidney

skeletal muscle

liver

lung

spleen

brain

heart

●

•

[illegible]

Fig. 5A

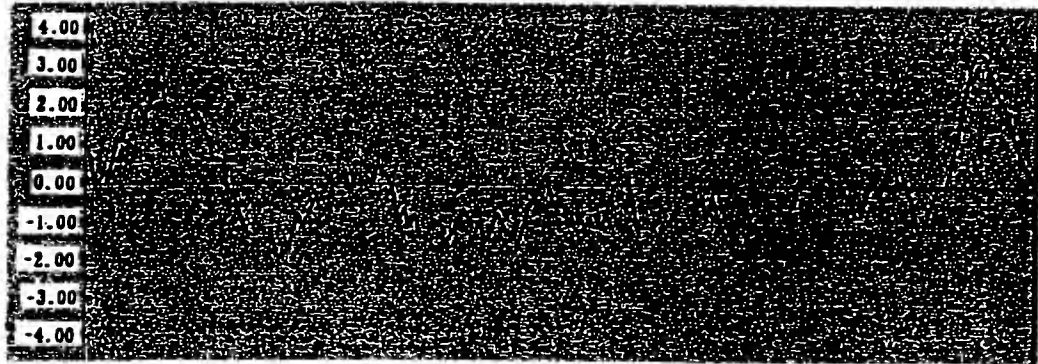


Fig. 5B

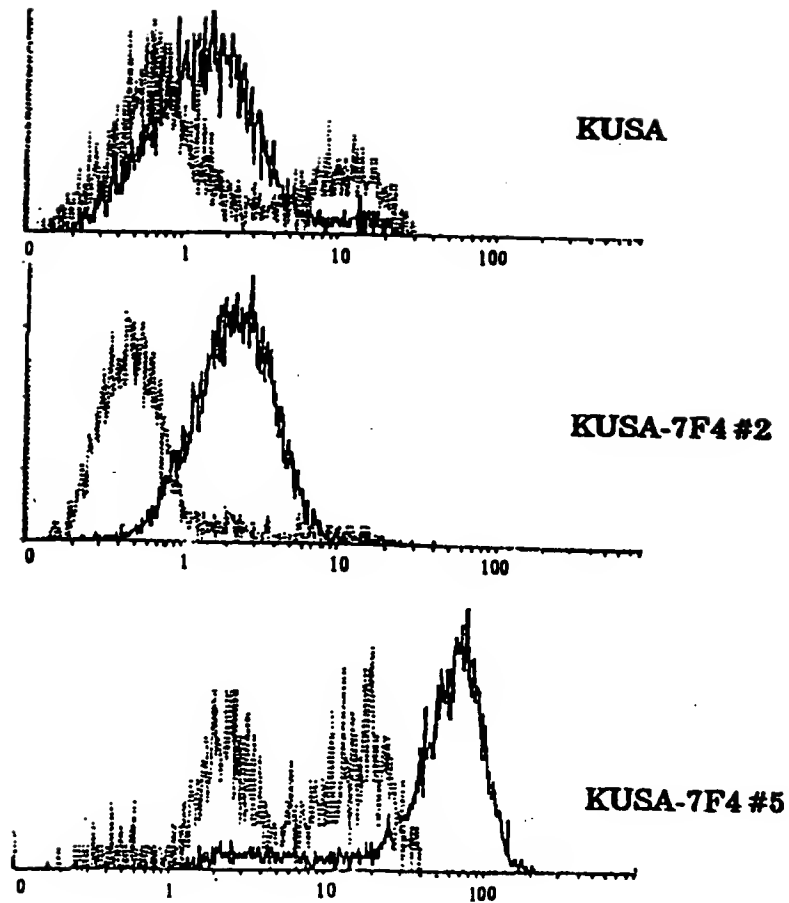


Fig. 6

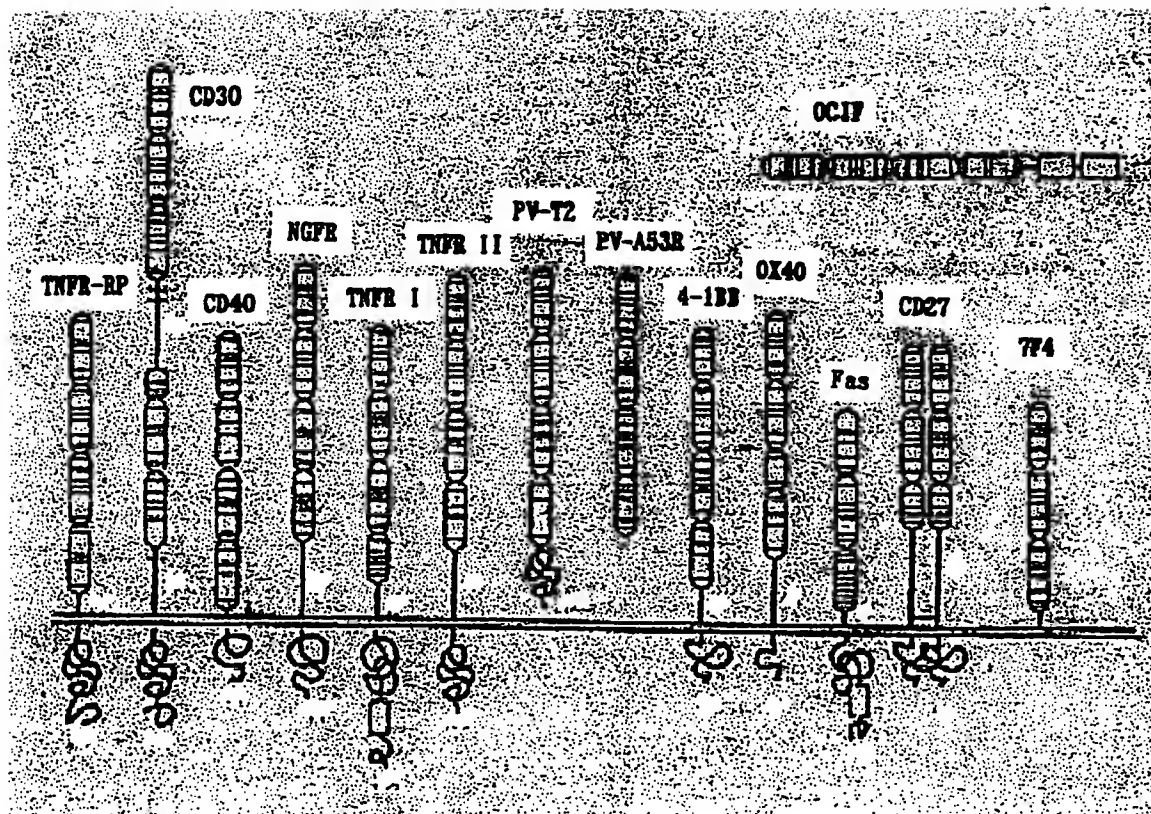


Fig. 7

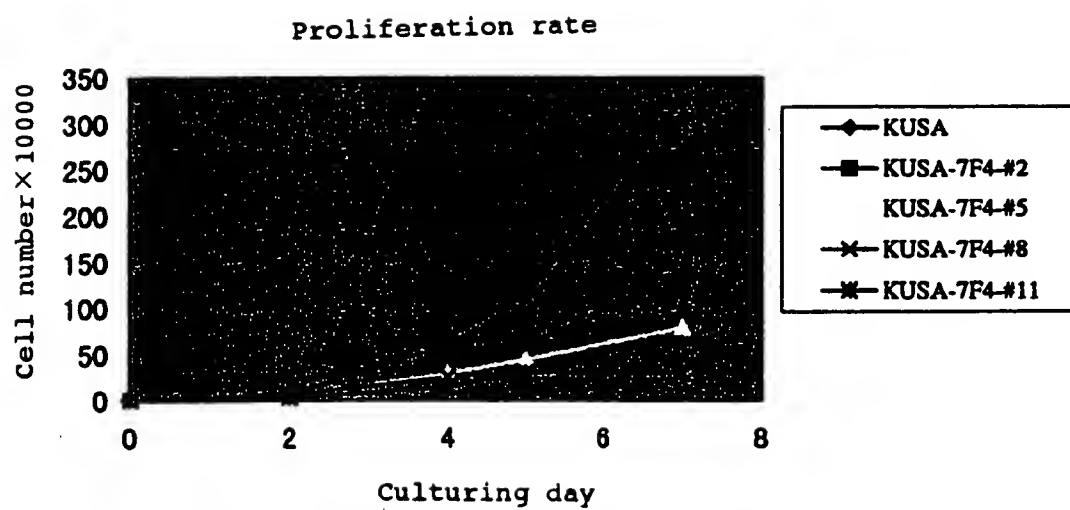


Fig. 8

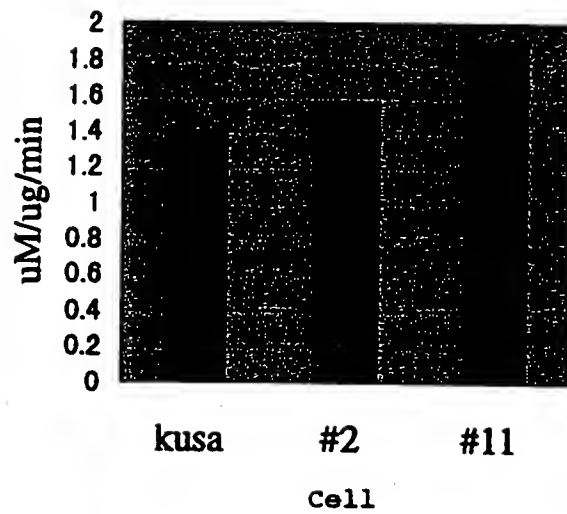


Fig. 9

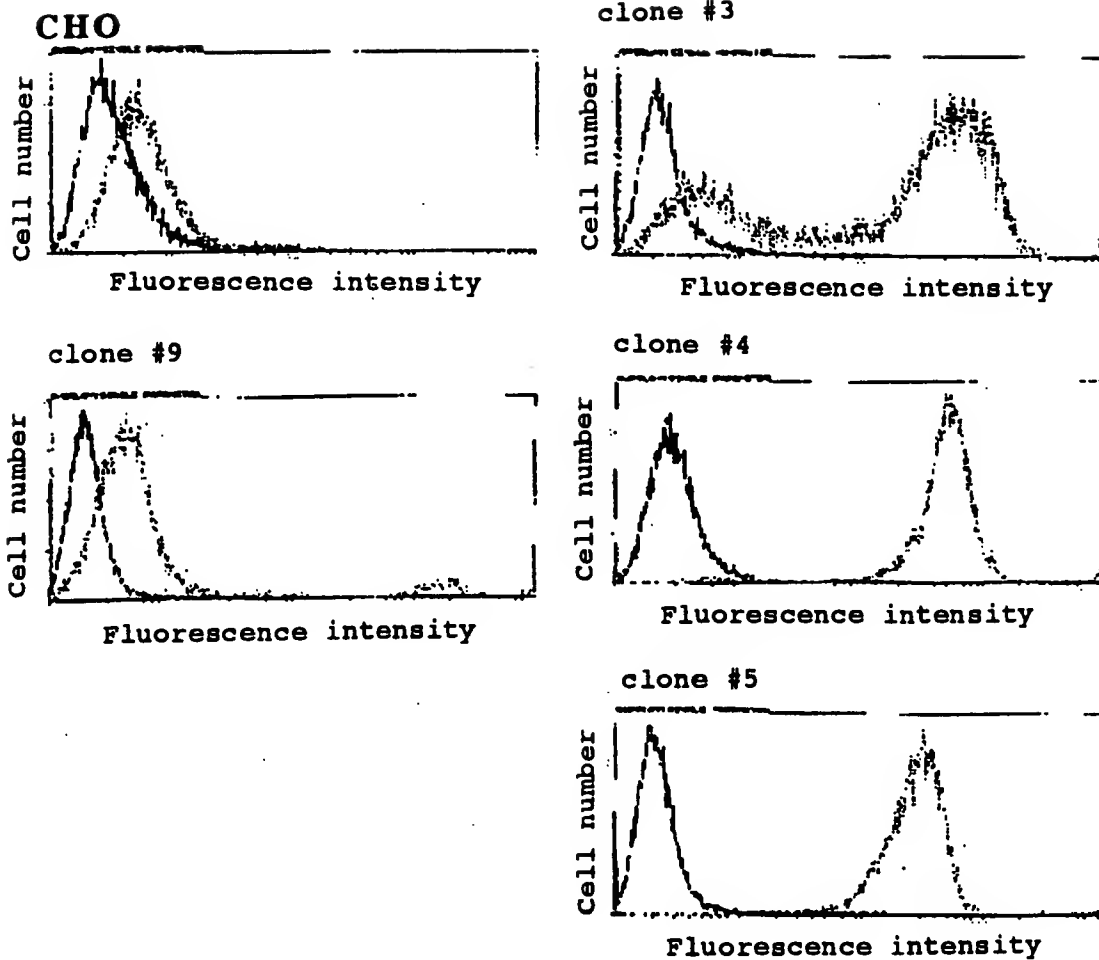


Fig. 10

